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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Hewick, Rodney M.  
Wang, Jack H.  
Wozney, John M.  
Celeste, Anthony J.

(ii) TITLE OF INVENTION: BONE AND CARTILAGE INDUCTIVE PROTEINS

(iii) NUMBER OF SEQUENCES: 44

C 3  
(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Legal Affairs - Genetics Institute, Inc.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/319,831  
(B) FILING DATE: 06-OCT-1994  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kapinos, Ellen J.  
(B) REGISTRATION NUMBER: 32,245  
(C) REFERENCE/DOCKET NUMBER: GI 5182A-DIV

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 498-8622  
(B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

42

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(F) TISSUE TYPE: Bone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp  
1 5 10 15

Val Ile Ala Pro Gln Gly Tyr  
20

C7  
(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bos taurus

(F) TISSUE TYPE: Bone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile  
1 5 10 15

Leu Arg

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

43

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bos taurus*

(F) TISSUE TYPE: Bone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Cys Cys Ala Pro Thr Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bos taurus*

(F) TISSUE TYPE: Bone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp  
1 5 10 15

Val His Gly Ser His Gly Arg  
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

44

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bos taurus

(vii) IMMEDIATE SOURCE:

(B) CLONE: acc30

(viii) POSITION IN GENOME:

(C) UNITS: bp

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 25..57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC

Lys Leu Ser Ala Thr Ser Val Leu Tyr  
1 5

51

TAC GAC AGCAGCAACA ATGTAATTCT AGA

Tyr Asp

10

80

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bos taurus*

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: Bovine genomic

(B) CLONE: Lambda 9800-10

## (viii) POSITION IN GENOME:

(C) UNITS: bp

## (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 20..99

## (ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 1..19

## (ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 100..119

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 22..99

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCTTGCGTG TCCCCGCAGA C GAC GTC CAC GGC TCC CAC GGC CGG CAG GTG 51

Asp Val His Gly Ser His Gly Arg Gln Val

1

5

10

TGC CGT CGG CAC GAG CTG TAC GTG AGC TTC CAG GAC CTG GGC TGG CTG 99

Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu

15

20

25

GTGAGTTCCG ACTCTCTTT 119

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His Glu Leu

49

1            5            10            15

Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu

20                      25

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens  
 (F) TISSUE TYPE: Human Heart

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human heart cDNA library stratagene catalog  
 (B) CLONE: hH38

## (viii) POSITION IN GENOME:

- (C) UNITS: bp

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 8..850

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 427..843

## (ix) FEATURE:

- (A) NAME/KEY: mRNA  
 (B) LOCATION: 1..997

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC    49  
 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile  
 -139            -135            -130

CCG GCT GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG    97  
 Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val  
 -125            -120            -115            -110

CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG    145

50

Pro Ser Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln  
 -105 -100 -95

GTG GTC CAG GAG CAG TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT 193  
 Val Val Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp  
 -90 -85 -80

CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG CTG GTG CTC GAT GTC 241  
 Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val  
 -75 -70 -65

ACA GCA GCC AGT GAC TGC TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA 289  
 Thr Ala Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly  
 -60 -55 -50

CTC CGC CTC TAT GTG GAG ACT GAG GAT GGG CAC AGC GTG GAT CCT GGC 337  
 Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly  
 -45 -40 -35 -30

CTG GCC GGC CTG CTG GGT CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC 385  
 Leu Ala Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe  
 -25 -20 -15

GTG GTC ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG 433  
 Val Val Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg  
 -10 -5 1

GCA GTG AGG CCA CTG AGG AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG 481  
 Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu  
 5 10 15

CCG CAG GCC AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC 529  
 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser  
 20 25 30 35

CAC GGC CGG CAG GTC TGC CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG 577  
 His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln  
 40 45 50

GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAA GGC TAC TCA GCC 625  
 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala  
 55 60 65

TAT TAC TGT GAG GGG GAG TGC TCC TTC CCG CTG GAC TCC TGC ATG AAC 673  
 Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn  
 70 75 80

GCC ACC AAC CAC GCC ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA 721  
 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro  
 85 90 95

51

AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC 769  
 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr  
 100 105 110 115

TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC 817  
 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His  
 120 125 130

CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCCCGCCCAGCCC 870  
 Arg Asn Met Val Val Lys Ala Cys Gly Cys His  
 135 140

TACTGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAACCCTTAAATGC 930

TGTCACAGCT CAAGCAGGAG TGTCAGGGGC CCTCACTCTC GGTGCCTACTTCCTGTCAGG 990

CTTCTGGGAA TTC 1003

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala  
 -139 -135 -130 -125

Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser  
 -120 -115 -110

Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val  
 -105 -100 -95

Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln  
 -90 -85 -80

Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala  
 -75 -70 -65 -60

Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg  
 -55 -50 -45

Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala  
 -40 -35 -30



52

Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val  
-25 -20 -15

Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val  
-10 -5 1 5

Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln  
10 15 20

Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly  
25 30 35

Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu  
40 45 50

Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr  
55 60 65

Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr  
70 75 80 85

Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala  
90 95 100

Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val  
105 110 115

Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn  
120 125 130

Met Val Val Lys Ala Cys Gly Cys His  
135 140

## (2) INFORMATION FOR SEQ ID NO:15:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

### (ii) MOLECULE TYPE: peptide

### (iii) HYPOTHETICAL: NO

### (iv) ANTI-SENSE: NO

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Val His Gly S r His Gly Arg Gln Val Cys Arg Arg His Glu Leu  
1 5 10 15

53

Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro  
20 25 30

Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu  
35 40 45

Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val  
50 55 60

His Leu Leu Lys Pro His Ala Val Pro Lys Ala Cys Cys Ala Pro Thr  
65 70 75 80

Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val  
85 90 95

Ile Leu Arg Lys His Arg Asn Met Val Val Arg Ala Cys Gly Cys His  
100 105 110

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp  
1 5 10 15

Ile Val Ala Pro Pro Gly Tyr  
20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser Glu Trp  
1 5 10 15

54

Ile Ile Ser Pro Lys Ser Phe

20

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp  
1 5 10 15

Ile Val Ala Pro Pro Gly Tyr  
20

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp  
1 5 10 15

Ile Ile Ala Pro Glu Gly Tyr  
20

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

55

Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp  
1 5 10 15

Ile Ile Ala Pro Lys Glu Tyr  
20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp  
1 5 10 15

Ile Ile Ala Pro Glu Gly Tyr  
20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val  
1 5 10 15

Leu Lys

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

56

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:**

Met Ser Ser Leu Ser Ile Leu Phe Phe Asp Glu Asn Lys Asn Val Val  
1 5 10 15

Leu Lys

**(2) INFORMATION FOR SEQ ID NO:24:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

**(ii) MOLECULE TYPE: peptide****(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:**

Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Tyr Asp Lys Val Val  
1 5 10 15

Leu Lys

**(2) INFORMATION FOR SEQ ID NO:25:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

**(ii) MOLECULE TYPE: peptide****(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:**

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Glu Val Ile  
1 5 10 15

Leu Lys

**(2) INFORMATION FOR SEQ ID NO:26:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

57

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile  
1 5 10 15

Leu Lys

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile  
1 5 10 15

Leu Lys

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ala Cys Cys Val Pro Thr Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids  
(B) TYPE: amino acid

46

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val His Leu Leu Lys Pro His Ala Val Pro Lys Ala Cys Cys Ala Pro  
 1 5 10 15

Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn  
 20 25 30

Val Ile Leu Arg Lys His Arg Asn Met Val Val Arg Ala Cys Gly Cys  
 35 40 45

His

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bos taurus

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Bovine genomic
- (B) CLONE: Lambda 9800-10

## (viii) POSITION IN GENOME:

- (C) UNITS: bp

## (ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 51..161

## (ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 1..50

## (ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 162..172

## (ix) FEATURE:

58

(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Pro Cys Cys Val Pro Glu Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala Cys Cys Val Pro Thr Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Pro Cys Cys Ala Pro Thr Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:



59

Pro Cys Cys Ala Pro Thr Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Pro Cys Cys Ala Pro Thr Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GACTCTAGAA TNACRTTRTT NGANG

25

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACTCTAGAA TNACRTTRTT NGARC

25

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GACTCTAGAA TNACRTTRTT RCTNG

25

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACTCTAGAA TNACRTTRTT RCTRC

25

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCGGATCCGC NTGYTCYGCN CCNAC

25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAGCTGAGCG CCACCTCCGT GCTCTACTAC

30

61

**(2) INFORMATION FOR SEQ ID NO:40:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 17 base pairs
- (B) TYPE:** nucleic acid
- (C) STRANDEDNESS:** unknown
- (D) TOPOLOGY:** unknown

**(ii) MOLECULE TYPE:** cDNA**(xi) SEQUENCE DESCRIPTION:** SEQ ID NO:40:

TGGGTNATHG CNCCNCA

17

**(2) INFORMATION FOR SEQ ID NO:41:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 17 base pairs
- (B) TYPE:** nucleic acid
- (C) STRANDEDNESS:** unknown
- (D) TOPOLOGY:** unknown

**(ii) MOLECULE TYPE:** cDNA**(xi) SEQUENCE DESCRIPTION:** SEQ ID NO:41:

ATHGCNCCNC ARGGNTA

17

**(2) INFORMATION FOR SEQ ID NO:42:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 30 base pairs
- (B) TYPE:** nucleic acid
- (C) STRANDEDNESS:** unknown
- (D) TOPOLOGY:** unknown

**(ii) MOLECULE TYPE:** cDNA**(xi) SEQUENCE DESCRIPTION:** SEQ ID NO:42:

GTCATCGCCC CCAAGGCTA CTCAGCCTAT

30

**(2) INFORMATION FOR SEQ ID NO:43:****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 24 base pairs
- (B) TYPE:** nucleic acid
- (C) STRANDEDNESS:** unknown
- (D) TOPOLOGY:** unknown

**(ii) MOLECULE TYPE:** cDNA

62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACGACGTCCA CGGCTCCCAC GGCC

24

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACGACGTCCA CGGCTCCCAC GGCC

24

C3